

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hammond, H. Kirk

Insel, Paul A.

Ping, Peipei

Post, Steven R.

Gao, Meihua

(ii) TITLE OF THE INVENTION: GENE THERAPY FOR CONGESTIVE
HEART FAILURE

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORRISON & FOERSTER
- (B) STREET: 755 PAGE MILL ROAD
- (C) CITY: PALO ALTO
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/472,667
- (B) FILING DATE: December 27, 1999

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: POLIZZI, CATHERINE M.
- (B) REGISTRATION NUMBER: 40,130
- (C) REFERENCE/DOCKET NUMBER: 220002056723

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-813-5600

(B) TELEFAX: 650-494-0792
 (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...312
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA
 48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC
 96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG
 144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC
 192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
 50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA NGC AAG GGC AAG
 240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys
 65 70 75 80

GAA CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAA GAT ACC GAA GTG

288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95

ACA ACG ACA CCG GCG GGA CCG CTG AA

314

Thr Thr Thr Pro Ala Gly Pro Leu
100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys

1 5 10 15

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly

20 25 30

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg

35 40 45

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro

50 55 60

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys

65 70 75 80

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

Thr Thr Thr Pro Ala Gly Pro Leu

100

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1812
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC GGG GGC GCT
48

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala
1 5 10 15

TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG TGC CCT GTG
96

Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val
20 25 30

TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC ATG CGG GCT 144
Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala

35 40 45

GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG ATC TTG GCC 192
Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala

50 55 60

TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG CTC GGT GCC
240

Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
65 70 75 80

AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC TGC ACA CAC
288

Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
85 90 95

TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG ACC CGC AGT
336

Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
100 105 110

TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG CAG CAG GAG
384

Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu

115 120 125

CGG CTG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG GAG ATG AAA
 432
 Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys
 130 135 140

GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG ATC TAC ATA
 480
 Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile
 145 150 155 160

CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT GAG GGC TTC
 528
 Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe
 165 170 175

ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC ATG ACC CTG
 576
 Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu
 180 185 190

AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG AAT CAC TGC
 624
 Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys
 195 200 205

CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG TCA GGG CTG
 672
 Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu
 210 215 220

CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG ATG GGG GTA
 720
 Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val
 225 230 235 240

GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA GGT GTG AAT
 768
 Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn
 245 250 255

GTC AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC TGC GGC GTC
 816
 Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val

260 265 270

CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT GAT GTG ACC
864

Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr
275 280 285

CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC ATC CAC ATC
912

Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile
290 295 300

ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA GTG GAG CCA
960

Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro
305 310 315 320

GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG CAC ATT GAG
1008

Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu
325 330 335

ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG GAG AAA GGC
1056

Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly
340 345 350

ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG GAA GGG CTG
1104

Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu
355 360 365

ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC AAG GAC TCC
1152

Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser
370 375 380

AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA GAC AAC CGG
1200

Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg
385 390 395 400

GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT GAG TTC CTG
1248

Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu

405 410 415

AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG AAG GAC CAT
1296

Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His
420 425 430

GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT GAG AAG AAG
1344

Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys
435 440 445

TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT GCC TGT GCC
1392

Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala
450 455 460

CTG TTG GTC TTC TGC TTC ATC TGC TTC ATC CAG CTT CTA ATT TTC CCA 1440
Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro
465 470 475 480

CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC CTG CTG CTG
1488

His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu
485 490 495

CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT TCT CTG TTC 1536
Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
500 505 510

CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC TCA CGG GCA
1584

Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
515 520 525

CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG TTT ACT TCT 1632
His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
530 535 540

GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA CGG AGC TGT
1680

Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
545 550 555 560

GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT GCC TGC CAC
1728

Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
565 570 575

CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC CTG TGT GAG
1776

Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu
580 585 590

GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TTC 1812
Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe
595 600

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala
1 5 10 15

Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val
20 25 30

Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala
35 40 45

Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala
50 55 60

Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
65 70 75 80

Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
85 90 95

Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
100 105 110

Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu
115 120 125

Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys

| | | |
|---|-----|-----|
| 130 | 135 | 140 |
| Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile | | |
| 145 | 150 | 155 |
| 160 | | |
| Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe | | |
| 165 | 170 | 175 |
| Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu | | |
| 180 | 185 | 190 |
| Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys | | |
| 195 | 200 | 205 |
| Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu | | |
| 210 | 215 | 220 |
| Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val | | |
| 225 | 230 | 235 |
| 240 | | |
| Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn | | |
| 245 | 250 | 255 |
| Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val | | |
| 260 | 265 | 270 |
| Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr | | |
| 275 | 280 | 285 |
| Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile | | |
| 290 | 295 | 300 |
| Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro | | |
| 305 | 310 | 315 |
| 320 | | |
| Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu | | |
| 325 | 330 | 335 |
| Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly | | |
| 340 | 345 | 350 |
| Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu | | |
| 355 | 360 | 365 |
| Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser | | |
| 370 | 375 | 380 |
| Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg | | |
| 385 | 390 | 395 |
| 400 | | |
| Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu | | |
| 405 | 410 | 415 |
| Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His | | |
| 420 | 425 | 430 |
| Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys | | |
| 435 | 440 | 445 |
| Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala | | |
| 450 | 455 | 460 |
| Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro | | |
| 465 | 470 | 475 |
| 480 | | |
| His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu | | |
| 485 | 490 | 495 |

Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
 500 505 510
 Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
 515 520 525
 His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
 530 535 540
 Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
 545 550 555 560
 Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
 565 570 575
 Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu
 580 585 590
 Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe
 595 600

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...3501
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA
 48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC
 96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG
 144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC
192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA GGC AAG GGC AAG
240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
65 70 75 80

GAG CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAG GAT ACC GAG GTG
288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95

ACA ACG ACA GCG GGC GGG ACG GCT GAG GTG GCG CCC GAC GCG GTG CCC
336

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
100 105 110

AGG AGT GGG CGA TCC TGC TGG CGC CGT TTG GTG CAG GTG TTC CAG TCG
384

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
115 120 125

AAG CAG TTC CGT TCG GCC AAG CTG GAG CGC CTG TAC CAG CGG TAC TTT
432

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
130 135 140

TTC CAG ATG AAC CAG AGC AGC CTG ACG CTG CTG GTG GCG GTG CTG GTG
480

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val
145 150 155 160

CTG CTC ACA GCG GTG CTG CTG GCT TTC CAA GCC GCA CCC GCC CGC CCT
528

Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro
165 170 175

CAG CCT GCC TAT GTG GCA CTG TTG GCC TGT GCC GCC CTG TTC GTG
576

Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Leu Phe Val
180 185 190

GGG CTC ATG GTG GTG TGT AAC CGG CAT AGC TTC CGC CAG GAC TCC ATG
624

Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
195 200 205

TGG GTG GTG AGT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC
672

Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
210 215 220

GGG GGC GCT TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG
720

Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
225 230 235 240

TGC CCT GTG TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC 768
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
245 250 255

ATG CGG GCT GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG
816

Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
260 265 270

ATC TTG GCC TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG
864

Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
275 280 285

CTC GGT GCC AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC 912
Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile
290 295 300

TGC ACA CAC TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG
960

Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
305 310 315 320

ACC CGC AGT TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG
1008

Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
325 330 335

CAG CAG GAG CGG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG
1056

Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met
340 345 350

GAG ATG AAA GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG
1104

Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys
355 360 365

ATC TAC ATA CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT
1152

Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile
370 375 380

GAG GGC TTC ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC
1200

Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val
385 390 395 400

ATG ACC CTG AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG
1248

Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu
405 410 415

AAT CAC TGC CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG
1296

Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val
420 425 430

TCA GGG CTG CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG
1344

Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu
435 440 445

ATG GGG GTA GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA
1392

Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr
450 455 460

GGT GTG AAT GTG AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC
1440

Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His
465 470 475 480

TGC GGC GTC CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT
1488

Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn
485 490 495

GAT GTG ACC CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC
1536

Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg
500 505 510

ATC CAC ATC ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA
1584

Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu
515 520 525

G TG GAG CCA GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG
1632

Val Glu Pro Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln
530 535 540

CAC ATT GAG ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG
1680

His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu
545 550 555 560

GAG AAA GGC ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG
1728

Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met
565 570 575

GAA GGG CTG ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC
1776

Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr
580 585 590

AAG GAC TCC AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA
1824

Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys
595 600 605

GAC AAC CGG GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT
1872

Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp
610 615 620

GAG TTC CTG AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG

1920

Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg
625 630 635 640

AAG GAC CAT GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT

1968

Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe
645 650 655

GAG AAG AAG TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT

2016

Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val
660 665 670

GCC TGT GCC CTG TTG GTC TTC TGC ATC TGC TTC ATC CAG CTT CTA 2064

Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu

675 680 685

ATT TTC CCA CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC 2112

Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe

690 695 700

CTG CTG CTG CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT

2160

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly
705 710 715 720

TCT CTG TTC CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC

2208

Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg
725 730 735

TCA CGG GCA CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG

2256

Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val
740 745 750

TTT ACT TCT GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA

2304

Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile
755 760 765

CGG AGC TGT GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT

2352

Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr
 770 775 780

GCC TGC CAC CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC
 2400
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro
 785 790 795 800

CTG TGT GAG GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TCC ATC
 2448
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile
 805 810 815

GGG AAC ATG CTG CTG AGT CTC TTG GCC AGC TCT GTC TTC CTG CAC ATC
 2496
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile
 820 825 830

AGC AGC ATC GGG AAG TTG GCC ATG ATC TTT GTC TTG GGG CTC ATC TAT
 2544
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr
 835 840 845

TTG GTG CTG CTT CTG CTG GGT CCC CCA GCC GCC ATC TTT GAC AAC TAT
 2592
 Leu Val Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr
 850 855 860

GAC CTA CTG CTT GGC GTC CAT GGC TTG GCT TCT TCC AAT GAG ACC TTT
 2640
 Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
 865 870 875 880

GAT GGG CTG GAC TGT CCA GCT GCA GGG AGG GTG GCC CTC AAA TAT ATG
 2688
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
 885 890 895

ACC CCT GTG ATT CTG CTG GTG TTT GCG CTG GCG CTG TAT CTG CAT GCT
 2736
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
 900 905 910

CAG CAG GTG GAA TCG ACT GCC CGC CTA AAC TTC CTC TGG AAA CTA CAG
 2784

Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln
 915 920 925

GCA ACA GGG GAA AAA GAG GAG ATG GAG GAG CTA CAG GCA TAC AAC CGG
 2832
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940

AGG CTG CTG CAT AAC ATT CTG CCC AAG GAC GTG GCG GCC CAC TTC CTG
 2880
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960

GCC CGG GAG CGC CGC AAT GAT GAA CTC TAC TAT CAG TCG TGT GAG TGT
 2928
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975

GTG GCT GTT ATG TTT GCC TCC ATT GCC AAC TTC TCT GAG TTC TAT GTG 2976
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990

GAG CTG GAG GCA AAC AAT GAG GGT GCC GAG TGC CTG CGG CTG CTC AAC
 3024
 Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Leu Asn
 995 1000 1005

GAG ATC ATC GCT TTT GAT GAG ATT ATC AGC GAG GAG CGG TTC CGG
 3072
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020

CAG CTG GAA AAG ATC AAG ACG ATT GGT AGC ACC TAC ATG GCT GCC TCA
 3120
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 1025 1030 1035 1040

GGG CTG AAC GCC AGC ACC TAC GAT CAG GTG GGC CGC TCC CAC ATC ACT
 3168
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055

GCC CTG GCT GAC TAC GCC ATG CGG CTC ATG GAG CAG ATG AAG CAC ATC
 3216
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

1060 1065 1070

AAT GAG CAC TCC TTC AAC AAT TTC CAG ATG AAG ATT GGG CTG AAC ATG
3264

Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met
1075 1080 1085

GGC CCA GTC GTG GCA GGT GTC ATC GGG GCT CGG AAG CCA CAG TAT GAC
3312

Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp
1090 1095 1100

ATC TGG GGG AAC ACA GTG AAT GTC TCT AGT CGT ATG GAC AGC ACG GGG
3360

Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly
1105 1110 1115 1120

GTC CCC GAC CGA ATC CAG GTG ACC ACG GAC CTG TAC CAG GTT CTA GCT
3408

Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala
1125 1130 1135

GCC AAG GGC TAC CAG CTG GAG TGT CGA GGG GTG GTC AAG GTG AAG GGC
3456

Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly
1140 1145 1150

AAG GGG GAG ATG ACC ACC TAC TTC CTC AAT GGG GGC CCC AGC AGT TAACA
3506

Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
1155 1160 1165

GGGCCAGCC ACAAAATTCACTGAAGGGAC CAAGGTGGGC ACT 3549

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
 50 55 60
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
 65 70 75 80
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
 85 90 95
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
 100 105 110
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
 115 120 125
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
 130 135 140
 Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val
 145 150 155 160
 Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro
 165 170 175
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Leu Phe Val
 180 185 190
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
 195 200 205
 Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
 210 215 220
 Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
 225 230 235 240
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
 245 250 255
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
 260 265 270
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile
 290 295 300
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320
 Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met

| | | |
|---|-----|-----|
| 340 | 345 | 350 |
| Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys | | |
| 355 | 360 | 365 |
| Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile | | |
| 370 | 375 | 380 |
| Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val | | |
| 385 | 390 | 395 |
| Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu | | |
| 405 | 410 | 415 |
| Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val | | |
| 420 | 425 | 430 |
| Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu | | |
| 435 | 440 | 445 |
| Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr | | |
| 450 | 455 | 460 |
| Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His | | |
| 465 | 470 | 475 |
| Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn | | |
| 485 | 490 | 495 |
| Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg | | |
| 500 | 505 | 510 |
| Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu | | |
| 515 | 520 | 525 |
| Val Glu Pro Gly Arg Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln | | |
| 530 | 535 | 540 |
| His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu | | |
| 545 | 550 | 555 |
| Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met | | |
| 565 | 570 | 575 |
| Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr | | |
| 580 | 585 | 590 |
| Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys | | |
| 595 | 600 | 605 |
| Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp | | |
| 610 | 615 | 620 |
| Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg | | |
| 625 | 630 | 635 |
| Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe | | |
| 645 | 650 | 655 |
| Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val | | |
| 660 | 665 | 670 |
| Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu | | |
| 675 | 680 | 685 |
| Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe | | |
| 690 | 695 | 700 |

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly
 705 710 715 720
 Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg
 725 730 735
 Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val
 740 745 750
 Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile
 755 760 765
 Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr
 770 775 780
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro
 785 790 795 800
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile
 805 810 815
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile
 820 825 830
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr
 835 840 845
 Leu Val Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr
 850 855 860
 Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
 865 870 875 880
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
 885 890 895
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
 900 905 910
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln
 915 920 925
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990
 Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Asn
 995 1000 1005
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 1025 1030 1035 1040
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

| | | |
|---|------|------|
| 1060 | 1065 | 1070 |
| Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met | | |
| 1075 | 1080 | 1085 |
| Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp | | |
| 1090 | 1095 | 1100 |
| Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly | | |
| 1095 | 1110 | 1115 |
| Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala | | |
| 1100 | 1125 | 1130 |
| Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly | | |
| 1115 | 1140 | 1145 |
| Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser | | |
| 1120 | 1145 | 1150 |
| 1135 | 1160 | 1165 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--------------------------------|----|
| ACGTAGAATT CGGRGAYTGT TAYTACTG | 28 |
|--------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | |
|----------------------------------|----|
| ACGTTAACGCT TCCASACRTC RAAYTGCCA | 29 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

UUAUUUAWW 9

<210> 10
<211> 3552
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(3507)

<400> SEQ ID NO:10
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Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
1 5 10 15

aca gcc tgg ggt gaa cgc aat ggg cag aag cgt tcg cgg cgc cgt ggc 96
Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
20 25 30

act cgg gca ggt ggc ttc tgc acg ccc cgc tat atg agc tgc ctc cgg 144
Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
35 40 45

gat gca gag cca ccc agc ccc acc cct gcg ggc ccc cct cgg tgc ccc 192
Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60

tgg cag gat gac gcc ttc atc cgg agg ggc ggc cca ggc aag ggc aag 240
Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
65 70 75 80

gag ctg ggg ctg cgg gca gtg gcc ctg ggc ttc gag gat acc gag gtg 288
Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

aca acg aca gcg ggc ggg acg gag gtg gcg ccc gac gcg gtg ccc 336
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
 100 105 110

agg agt ggg cga tcc tgc tgg cgc cgt ctg gtg cag gtg ttc cag tcg 384
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
 115 120 125

aag cag ttc cgt tcg gcc aag ctg gag cgc ctg tac cag cgg tac ttc 432
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
 130 135 140

ttc cag atg aac cag agc ctg acg ctg ctg atg gcg gtg ctg gtg 480
 Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val
 145 150 155 160

ctg ctc aca gcg gtg ctg ctg gct ttc cac gcc gca ccc gcc cgc cct 528
 Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro
 165 170 175

cag cct gcc tat gtg gca ctg ttg gcc tgt gcc gcc ctg ttc gtg 576
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Leu Phe Val
 180 185 190

ggg ctc atg gtg gtg tgt aac cgg cat agc ttc cgc cag gac tcc atg 624
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
 195 200 205

tgg gtg gtg agt tac gtg gtg ctg ggc atc ctg gcg gca gtg cag gtc 672
 Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
 210 215 220

ggg ggc gct ctc gca gca gac ccg cgc agc ccc tct gcg ggc ctc tgg 720
 Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
 225 230 235 240

tgc cct gtg ttc ttt gtc tac atc gcc tac acg ctc ctc ccc atc cgc 768
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
 245 250 255

atg cgg gct gcc gtc ctc agc ggc ctg ggc ctc tcc acc ttg cat ttg 816
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
 260 265 270

atc ttg gcc tgg caa ctt aac cgt ggt gat gcc ttc ctc tgg aag cag 864
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285

ctc ggt gcc aat gtg ctg ctg ttc ctc tgc acc aac gtc att ggc atc 912
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile
 290 295 300

tgc aca cac tat cca gca gag gtg tct cag cgc cag gcc ttt cag gag 960
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320

acc cgc ggt tac atc cag gcc cgg ctc cac ctg cag cat gag aat cgg 1008
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335

cag cag gag cgg ctg ctg tcg gta ttg ccc cag cac gtt gcc atg 1056
 Gln Gln Glu Arg Leu Leu Ser Val Leu Pro Gln His Val Ala Met
 340 345 350

gag atg aaa gaa gac atc aac aca aaa aaa gaa gac atg atg ttc cac 1104
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His
 355 360 365

aag atc tac ata cag aag cat gac aat gtc agc atc ctg ttt gca gac 1152
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp
 370 375 380

att gag ggc ttc acc agc ctg gca tcc cag tgc act gcg cag gag ctg 1200
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu
 385 390 395 400

gtc atg acc ctg aat gag ctc ttt gcc cgg ttt gac aag ctg gct gcg 1248
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala
 405 410 415

gag aat cac tgc ctg agg atc aag atc ttg ggg gac tgt tac tac tgt 1296
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys
 420 425 430

gtg tca ggg ctg ccg gag gcc cgg gcc gac cat gcc cac tgc tgt gtg 1344
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val
 435 440 445

gag atg ggg gta gac atg att gag gcc atc tcg ctg gta cgt gag gtg 1392
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val
 450 455 460

aca ggt gtg aat gtg aac atg cgc gtg ggc atc cac agc ggg cgc gtg 1440
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val
 465 470 475 480

cac tgc ggc gtc ctt ggc ttg cgg aaa tgg cag ttc gat gtg tgg tcc 1488
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser
 485 490 495

aat gat gtg acc ctg gcc aac cac atg gag gca gga ggc cgg gct ggc 1536
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Arg Ala Gly
 500 505 510

cgc atc cac atc act cgg gca aca ctg cag tac ctg aac ggg gac tac 1584
 Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr
 515 520 525

gag gtg gag cca ggc cgt ggt ggc gag cgc aac gcg tac ctc aag gag 1632
 Glu Val Glu Pro Gly Arg Gly Glu Arg Asn Ala Tyr Leu Lys Glu
 530 535 540

cag cac att gag act ttc ctc atc ctg ggc gcc agc cag aaa cgg aaa 1680
 Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys
 545 550 555 560

gag gag aag gcc atg ctg gcc aag ctg cag cgg act cgg gcc aac tcc 1728
 Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser
 565 570 575

atg gaa ggg ctg atg ccg cgc tgg gtt cct gat cgt gcc ttc tcc cgg 1776
 Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg
 580 585 590

acc aag gac tcc aag gcc ttc cgc cag atg ggc att gat gat tcc agc 1824
 Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser
 595 600 605

aaa gac aac cgg ggc acc caa gat gcc ctg aac cct gag gat gag gtg 1872
 Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val
 610 615 620

gat gag ttc ctg agc cgt gcc atc gat gcc cgc agc att gat cag ctg 1920

Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu
 625 630 635 640

cgg aag gac cat gtg cgc cgg ttt ctg ctc acc ttc cag aga gag gat 1968
 Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp
 645 650 655

ctt gag aag aag tac tcc cgg aag gtg gat ccc cgc ttc gga gcc tac 2016
 Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr
 660 665 670

gtt gcc tgt gcc ctg ttg gtc ttc atc tgc ttc atc cag ctt 2064
 Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu
 675 680 685

ctc atc ttc cca cac tcc acc ctg atg ctt ggg atc tat gcc agc atc 2112
 Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile
 690 695 700

ttc ctg ctg cta atc acc gtg ctg atc tgt gct gtg tac tcc tgt 2160
 Phe Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys
 705 710 715 720

ggt tct ctg ttc cct aag gcc ctg caa cgt ctg tcc cgc agc att gtc 2208
 Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val
 725 730 735

cgc tca cgg gca cat agc acc gca gtt ggc atc ttt tcc gtc ctg ctt 2256
 Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu
 740 745 750

gtg ttt act tct gcc att gcc aac atg ttc acc tgt aac cac acc ccc 2304
 Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro
 755 760 765

ata cgg agc tgt gca gcc cgg atg ctg aat tta aca cct gct gac atc 2352
 Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile
 770 775 780

act gcc tgc cac ctg cag cag ctc aat tac tct ctg ggc ctg gat gct 2400
 Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala
 785 790 795 800

ccc ctg tgt gag ggc acc atg ccc acc tgc agc ttt cct gag tac ttc 2448
 Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe

805 810 815

atc ggg aac atg ctg ctg agt ctc ttg gcc agc tct gtc ttc ctg cac 2496
Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His
820 825 830

atc agc agc atc ggg aag ttg gcc atg atc ttt gtc ttg ggg ctc atc 2544
Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile
835 840 845

tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc acc atc ttt gac aac 2592
Tyr Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn
850 855 860

tat gac cta ctg ctt ggc gtc cat ggc ttg gct tct tcc aat gag acc 2640
Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr
865 870 875 880

ttt gat ggg ctg gac tgt cca gct gca ggg agg gtg gcc ctc aaa tat 2688
Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr
885 890 895

atg acc cct gtg att ctg ctg gtg ttt gcg ctg gcg ctg tat ctg cat 2736
Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His
900 905 910

gct cag cag gtg gag tcg act gcc cgc cta gac ttc ctc tgg aaa cta 2784
Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu
915 920 925

cag gca aca ggg gag aag gag gag atg gag gag cta cag gca tac aac 2832
 Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn
 930 935 940

cgaggctgctgcataaacattctgccc aag gac gtggcgcccac ttc 2880
Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe
945 950 955 960

ctg gcc cg^c gag cgc cgc aat gat gaa ctc tac tat cag tcg tgt gag 2928
Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu
965 970 975

tgt gtg gct gtt atg ttt gcc tcc att gcc aac ttc tct gag ttc tat 2976
Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr
980 985 990

gtg gag ctg gag gca aac aat gag ggt gtc gag tgc ctg cgg ctg ctc 3024
 Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu
 995 1000 1005

aac gag atc atc gct gac ttt gat gag att atc agc gag gag cgg ttc 3072
 Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe
 1010 1015 1020

cgg cag ctg gaa aag atc aag acg att ggt agc acc tac atg gct gcc 3120
 Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala
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tca ggg ctg aac gcc agc acc tac gat cag gtg ggc cgc tcc cac atc 3168
 Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile
 1045 1050 1055

act gcc ctg gct gac tac gcc atg cgg ctc atg gag cag atg aag cac 3216
 Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His
 1060 1065 1070

atc aat gag cac tcc ttc aac aat ttc cag atg aag att ggg ctg aac 3264
 Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn
 1075 1080 1085

atg ggc cca gtc gtg gca ggt gtc atc ggg gct cgg aag cca cag tat 3312
 Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr
 1090 1095 1100

gac atc tgg ggg aac aca gtg aat gtc tct agt cgt atg gac agc acg 3360
 Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr
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ggg gtc ccc gac cga atc cag gtg acc acg gac ctg tac cag gtt cta 3408
 Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu
 1125 1130 1135

gct gcc aag ggc tac cag ctg gag tgt cga ggg gtg gtc aag gtg aag 3456
 Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys
 1140 1145 1150

ggc aag ggg gag atg acc acc tac ttc ctc aat ggg ggc ccc agc agt 3504
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Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
35 40 45
Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60
Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Pro Gly Lys Gly Lys
65 70 75 80
Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95
Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
100 105 110
Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
115 120 125
Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
130 135 140
Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val
145 150 155 160
Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro
165 170 175
Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Leu Phe Val
180 185 190
Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
195 200 205
Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
210 215 220
Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
225 230 235 240
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
245 250 255
Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
260 265 270
Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln

| | | |
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| 275 | 280 | 285 |
| Leu Gly Ala Asn Val Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile | | |
| 290 | 295 | 300 |
| Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu | | |
| 305 | 310 | 315 |
| Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg | | |
| 325 | 330 | 335 |
| Gln Gln Glu Arg Leu Leu Ser Val Leu Pro Gln His Val Ala Met | | |
| 340 | 345 | 350 |
| Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His | | |
| 355 | 360 | 365 |
| Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp | | |
| 370 | 375 | 380 |
| Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu | | |
| 385 | 390 | 395 |
| Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala | | |
| 405 | 410 | 415 |
| Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys | | |
| 420 | 425 | 430 |
| Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val | | |
| 435 | 440 | 445 |
| Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val | | |
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| Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val | | |
| 465 | 470 | 475 |
| His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser | | |
| 485 | 490 | 495 |
| Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Arg Ala Gly | | |
| 500 | 505 | 510 |
| Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr | | |
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| Glu Val Glu Pro Gly Arg Gly Glu Arg Asn Ala Tyr Leu Lys Glu | | |
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| Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys | | |
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| Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser | | |
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| Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg | | |
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| Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser | | |
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| Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val | | |
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| Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu | | |
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Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp
 645 650 655
 Leu Glu Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr
 660 665 670
 Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu
 675 680 685
 Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile
 690 695 700
 Phe Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys
 705 710 715 720
 Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val
 725 730 735
 Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu
 740 745 750
 Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro
 755 760 765
 Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile
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 Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His
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 Tyr Leu Val Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn
 850 855 860
 Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr
 865 870 875 880
 Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr
 885 890 895
 Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His
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 Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu
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 Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn
 930 935 940
 Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe
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 965 970 975
 Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr
 980 985 990
 Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu

| | | |
|---|------|----------------|
| 995 | 1000 | 1005 |
| Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe | | |
| 1010 | 1015 | 1020 |
| Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala | | |
| 1025 | 1030 | 1035 1040 |
| Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile | | |
| 1045 | 1050 | 1055 |
| Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His | | |
| 1060 | 1065 | 1070 |
| Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn | | |
| 1075 | 1080 | 1085 |
| Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr | | |
| 1090 | 1095 | 1100 |
| Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr | | |
| 1105 | 1110 | 1115 1120 |
| Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu | | |
| 1125 | 1130 | 1135 |
| Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys | | |
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| Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser | | |
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1 5 10

a a a g t g g a t g a a c g g a a a a c a g c c t g g g g t g a a c g c a a t g g g c a g a a g 99
Lys Val Asp Glu Arg Lys Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys
15 20 25

c g t t c g c g g c g c c g t g g c a c t c g g g c a g g t g g c t t c t g c a c g c c c c g c 147

Arg Ser Arg Arg Arg Gly Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg
 30 35 40

tat atg agc tgc ctc cgg gat gca gag cca ccc agc ccc acc cct gcg 195
 Tyr Met Ser Cys Leu Arg Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala
 45 50 55

ggc ccc cct cgg tgc ccc tgg cag gat gac gcc ttc atc cgg agg ggc 243
 Gly Pro Pro Arg Cys Pro Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly
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ggc cca ggc aag ggc aag gag ctg ggg ctg cgg gca gtg gcc ctg ggc 291
 Gly Pro Gly Lys Gly Lys Glu Leu Gly Leu Arg Ala Val Ala Leu Gly
 75 80 85 90

ttc gag gat acc gag gtg aca acg aca gcg ggc ggg acg gct gag gtg 339
 Phe Glu Asp Thr Glu Val Thr Thr Ala Gly Gly Thr Ala Glu Val
 95 100 105

gcg ccc gac gcg gtg ccc agg agt ggg cga tcc tgc tgg cgc cgt ctg 387
 Ala Pro Asp Ala Val Pro Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu
 110 115 120

gtg cag gtg ttc cag tcg aag cag ttc cgt tcg gcc aag ctg gag cgc 435
 Val Gln Val Phe Gln Ser Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg
 125 130 135

ctg tac cag cgg tac ttc ttc cag atg aac cag agc agc ctg acg ctg 483
 Leu Tyr Gln Arg Tyr Phe Phe Gln Met Asn Gln Ser Ser Leu Thr Leu
 140 145 150

ctg atg gcg gtg ctg gtg ctg ctc aca gcg gtg ctg ctg gct ttc cac 531
 Leu Met Ala Val Leu Val Leu Leu Thr Ala Val Leu Leu Ala Phe His
 155 160 165 170

gcc gca ccc gcc cgc cct cag cct gcc tat gtg gca ctg ttg gcc tgt 579
 Ala Ala Pro Ala Arg Pro Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys
 175 180 185

gcc gcc gcc ctg ttc gtg ggg ctc atg gtg gtg tgt aac cgg cat agc 627
 Ala Ala Ala Leu Phe Val Gly Leu Met Val Val Cys Asn Arg His Ser
 190 195 200

ttc cgc cag gac tcc atg tgg gtg gtg agt tac gtg gtg ctg ggc atc 675
 Phe Arg Gln Asp Ser Met Trp Val Val Ser Tyr Val Val Leu Gly Ile

205 210 215

ctg gcg gca gtg cag gtc ggg ggc gct ctc gca gca gac ccg cgc agc 723
 Leu Ala Ala Val Gln Val Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser
 220 225 230

ccc tct gcg ggc ctc tgg tgc cct gtg ttc ttt gtc tac atc gcc tac 771
 Pro Ser Ala Gly Leu Trp Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr
 235 240 245 250

acg ctc ctc ccc atc cgc atg cgg gct gcc gtc ctc agc ggc ctg ggc 819
 Thr Leu Leu Pro Ile Arg Met Arg Ala Ala Val Leu Ser Gly Leu Gly
 255 260 265

ctc tcc acc ttg cat ttg atc ttg gcc tgg caa ctt aac cgt ggt gat 867
 Leu Ser Thr Leu His Leu Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp
 270 275 280

gcc ttc ctc tgg aag cag ctc ggt gcc aat gtg ctg ctg ttc ctc tgc 915
 Ala Phe Leu Trp Lys Gln Leu Gly Ala Asn Val Leu Leu Phe Leu Cys
 285 290 295

acc aac gtc att ggc atc tgc aca cac tat cca gca gag gtg tct cag 963
 Thr Asn Val Ile Gly Ile Cys Thr His Tyr Pro Ala Glu Val Ser Gln
 300 305 310

cgc cag gcc ttt cag gag acc cgc ggt tac atc cag gcc cgg ctc cac 1011
 Arg Gln Ala Phe Gln Glu Thr Arg Gly Tyr Ile Gln Ala Arg Leu His
 315 320 325 330

ctg cag cat gag aat cgg cag cag gag cgg ctg ctg tcg gta ttg 1059
 Leu Gln His Glu Asn Arg Gln Gln Glu Arg Leu Leu Leu Ser Val Leu
 335 340 345

ccc cag cac gtt gcc atg gag atg aaa gaa gac atc aac aca aaa aaa 1107
 Pro Gln His Val Ala Met Glu Met Lys Glu Asp Ile Asn Thr Lys Lys
 350 355 360

gaa gac atg atg ttc cac aag atc tac ata cag aag cat gac aat gtc 1155
 Glu Asp Met Met Phe His Lys Ile Tyr Ile Gln Lys His Asp Asn Val
 365 370 375

agc atc ctg ttt gca gac att gag ggc ttc acc agc ctg gca tcc cag 1203
 Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln
 380 385 390

tgc act gcg cag gag ctg gtc atg acc ttg aat gag ctc ttt gcc cg 1251
 Cys Thr Ala Gln Glu Leu Val Met Thr Leu Asn Glu Leu Phe Ala Arg
 395 400 405 410

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 Phe Asp Lys Leu Ala Ala Glu Asn His Cys Leu Arg Ile Lys Ile Leu
 415 420 425

gga gac tgt tac tac tgc gtg tca ggg ctg ccc gag gcc cg gca gat 1347
 Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu Pro Glu Ala Arg Ala Asp
 430 435 440

cac gcc cac tgc tgt gtg gag atg ggg gta gac atg atc gaa gcc atc 1395
 His Ala His Cys Cys Val Glu Met Gly Val Asp Met Ile Glu Ala Ile
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tcg ctg gtg cgt gag gta aca ggt gtg aac atg cgt gtg ggc 1443
 Ser Leu Val Arg Glu Val Thr Gly Val Asn Val Asn Met Arg Val Gly
 460 465 470

atc cac agc gga cgt gtg cat tgc ggc gtc ctt ggc cta cgg aaa tgg 1491
 Ile His Ser Gly Arg Val His Cys Gly Val Leu Gly Leu Arg Lys Trp
 475 480 485 490

cag ttt gat gtc tgg tca aac gat gtg acc ctg gct aac cac atg gag 1539
 Gln Phe Asp Val Trp Ser Asn Asp Val Thr Leu Ala Asn His Met Glu
 495 500 505

gcc ggg ggc ggc cgg cgc atc cac atc act cgg gct aca ctg cag tac 1587
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 510 515 520

ttg aac ggg gac tat gag gtg gag cca ggc cgt ggt ggt gaa cgc aat 1635
 Leu Asn Gly Asp Tyr Glu Val Glu Pro Gly Arg Gly Glu Arg Asn
 525 530 535

gcg tac ctc aag gag cag tgc att gag acc ttc ctc ata ctt ggc gcc 1683
 Ala Tyr Leu Lys Glu Gln Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala
 540 545 550

agc caa aaa cgg aaa gag gag aaa gcc atg ctg gcc aag ctt cag cgg 1731
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 555 560 565 570

aca cg ggc aac tcc atg gaa gga ctg atg ccc cgc tgg gtt cct gac 1779
 Thr Arg Ala Asn Ser Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp
 575 580 585

cgt gcc ttc tcc cgg acc aag gac tct aag gca ttc cgc cag atg ggc 1827
 Arg Ala Phe Ser Arg Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly
 590 595 600

att gat gat tct agc aaa gac aac cgg ggt gcc caa gat gct ctg aac 1875
 Ile Asp Asp Ser Ser Lys Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn
 605 610 615

cct gaa gat gag gtg gat gag ttc ctg ggc cga gcc atc gat gcc cgc 1923
 Pro Glu Asp Glu Val Asp Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg
 620 625 630

agc att gat cag ctg cgg aag gac cat gtg cgc cgg ttt ctg ctc acc 1971
 Ser Ile Asp Gln Leu Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr
 635 640 645 650

ttc cag aga gag gat ctt gag aag aag tac tcc cgg aag gtg gat ccc 2019
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 655 660 665

cgc ttc gga gcc tac gtt gcc tgt gtc ttg gtc ttc tgc atc 2067
 Arg Phe Gly Ala Tyr Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile
 670 675 680

tgc ttc atc cag ctt ctc atc ttc cca cac tcc acc ctg atg ctt ggg 2115
 Cys Phe Ile Gln Leu Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly
 685 690 695

atc tat gcc agc atc ttc ctg ctg cta atc acc gtg ctg atc tgt 2163
 Ile Tyr Ala Ser Ile Phe Leu Leu Leu Ile Thr Val Leu Ile Cys
 700 705 710

gct gtg tac tcc tgt ggt tct ctg ttc cct aag gcc ctg caa cgt ctg 2211
 Ala Val Tyr Ser Cys Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu
 715 720 725 730

tcc cgc agc att gtc cgc tca cgg gca cat agc acc gca gtt ggc atc 2259
 Ser Arg Ser Ile Val Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile
 735 740 745

ttt tcc gtc ctg ctt gtg ttt act tct gcc att gcc aac atg ttc acc 2307

Phe Ser Val Leu Leu Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr
 750 755 760

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 765 770 775

aca cct gct gac atc act gcc tgc cac ctg cag cag ctc aat tac tct 2403
 Thr Pro Ala Asp Ile Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser
 780 785 790

ctg ggc ctg gat gct ccc ctg tgt gag ggc acc atg ccc acc tgc agc 2451
 Leu Gly Leu Asp Ala Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser
 795 800 805 810

ttt cct gag tac ttc atc ggg aac atg ctg ctg agt ctc ttg gcc agc 2499
 Phe Pro Glu Tyr Phe Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser
 815 820 825

tct gtc ttc ctg cac atc agc agc atc ggg aag ttg gcc atg atc ttt 2547
 Ser Val Phe Leu His Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe
 830 835 840

gtc ttg ggg ctc atc tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc 2595
 Val Leu Gly Leu Ile Tyr Leu Val Leu Leu Leu Gly Pro Pro Ala
 845 850 855

acc atc ttt gac aac tat gac cta ctg ctt ggc gtc cat ggc ttg gct 2643
 Thr Ile Phe Asp Asn Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala
 860 865 870

tct tcc aat gag acc ttt gat ggg ctg gac tgt cca gct gca ggg agg 2691
 Ser Ser Asn Glu Thr Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg
 875 880 885 890

gtg gcc ctc aaa tat atg acc cct gtg att ctg ctg gtg ttt gcg ctg 2739
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925 930 935

cta cag gca tac aac cgg agg ctg ctg cat aac att ctg ccc aag gac 2883
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 940 945 950

gtg gcg gcc cac ttc ctg gcc cgg gag cgc cgc aat gat gaa ctc tac 2931
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 955 960 965 970

tat cag tcg tgt gag tgt gct gtt atg ttt gcc tcc att gcc aac 2979
 Tyr Gln Ser Cys Glu Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn
 975 980 985

ttc tct gag ttc tat gtg gag ctg gag gca aac aat gag ggt gtc gag 3027
 Phe Ser Glu Phe Tyr Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu
 990 995 1000

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 1005 1010 1015

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 1020 1025 1030

acc tac atg gct gcc tca ggg ctg aac gcc agc acc tac gat cag gtg 3171
 Thr Tyr Met Ala Ala Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val
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 1070 1075 1080

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 Lys Ile Gly Leu Asn Met Gly Pro Val Val Ala Gly Val Ile Gly Ala
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cgg aag cca cag tat gac atc tgg ggg aac aca gtg aat gtc tct agt 3363
 Arg Lys Pro Gln Tyr Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser
 1100 1105 1110

cgt atg gac agc acg ggg gtc ccc gac cga atc cag gtg acc acg gac 3411
 Arg Met Asp Ser Thr Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp
 1115 1120 1125 1130

ctg tac cag gtt cta gct gcc aag ggc tac cag ctg gag tgt cga ggg 3459
 Leu Tyr Gln Val Leu Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly
 1135 1140 1145

gtg gtc aag gtg aag ggc aag ggg gag atg acc acc tac ttc ctc aat 3507
 Val Val Lys Val Lys Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn
 1150 1155 1160

ggg ggc ccc agc agt taa caggccccag ccacaaattc agctgaaggg 3555
 Gly Gly Pro Ser Ser
 1165

accaaggtgg gcactaaggg cgaattc 3582

<210> 13

<211> 1167

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified AC-VI

<400> SEQ ID NO:13

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys

1 5 10 15

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly

20 25 30

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg

35 40 45

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro

50 55 60

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys

65 70 75 80

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro

100 105 110

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser

115 120 125

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe

130 135 140

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val
 145 150 155 160
 Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro
 165 170 175
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val
 180 185 190
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
 195 200 205
 Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
 210 215 220
 Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
 225 230 235 240
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
 245 250 255
 Met Arg Ala Ala Val Leu Ser Gly Leu Ser Thr Leu His Leu
 260 265 270
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile
 290 295 300
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335
 Gln Gln Glu Arg Leu Leu Ser Val Leu Pro Gln His Val Ala Met
 340 345 350
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His
 355 360 365
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp
 370 375 380
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu
 385 390 395 400
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala
 405 410 415
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys
 420 425 430
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val
 435 440 445
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val
 450 455 460
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val
 465 470 475 480
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser
 485 490 495
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Arg Arg

| | | |
|---|-----|-----|
| 500 | 505 | 510 |
| Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu | | |
| 515 | 520 | 525 |
| Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu Gln | | |
| 530 | 535 | 540 |
| Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu | | |
| 545 | 550 | 555 |
| Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met | | |
| 565 | 570 | 575 |
| Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr | | |
| 580 | 585 | 590 |
| Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys | | |
| 595 | 600 | 605 |
| Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp | | |
| 610 | 615 | 620 |
| Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg | | |
| 625 | 630 | 635 |
| Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Leu | | |
| 645 | 650 | 655 |
| Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val | | |
| 660 | 665 | 670 |
| Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu | | |
| 675 | 680 | 685 |
| Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe | | |
| 690 | 695 | 700 |
| Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly | | |
| 705 | 710 | 715 |
| Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg | | |
| 725 | 730 | 735 |
| Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val | | |
| 740 | 745 | 750 |
| Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile | | |
| 755 | 760 | 765 |
| Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr | | |
| 770 | 775 | 780 |
| Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro | | |
| 785 | 790 | 795 |
| Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe Ile | | |
| 805 | 810 | 815 |
| Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile | | |
| 820 | 825 | 830 |
| Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr | | |
| 835 | 840 | 845 |
| Leu Val Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn Tyr | | |
| 850 | 855 | 860 |

Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
 865 870 875 880
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
 885 890 895
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
 900 905 910
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu Gln
 915 920 925
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990
 Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu Asn
 995 1000 1005
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 1025 1030 1035 1040
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile
 1060 1065 1070
 Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met
 1075 1080 1085
 Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp
 1090 1095 1100
 Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly
 1105 1110 1115 1120
 Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala
 1125 1130 1135
 Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly
 1140 1145 1150
 Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
 1155 1160 1165